

#13

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/750,590

DATE: 09/21/2001
TIME: 18:46:17

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\09212001\I750590.raw

ENTERED

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4 <110> APPLICANT: Ira Herman
5 Alice Welch
7 <120> TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL AND
8 ABNORMAL CELL MIGRATION
10 <130> FILE REFERENCE: TUI-001CP
12 <140> CURRENT APPLICATION NUMBER: US 09/750,590
13 <141> CURRENT FILING DATE: 2000-12-28
15 <150> PRIOR APPLICATION NUMBER: 60/170,182
16 <151> PRIOR FILING DATE: 1999-12-10
18 <150> PRIOR APPLICATION NUMBER: 09/733,818
19 <151> PRIOR FILING DATE: 2000-12-08
21 <160> NUMBER OF SEQ ID NOS: 3
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 4730
27 <212> TYPE: DNA
28 <213> ORGANISM: Bos taurus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (392)...(4597)
34 <400> SEQUENCE: 1
35 cagtgttgag gcggcaggat gtagagtgcgt gttcaagctt tccagtggag tccccgaaaa 60
36 gggaaggcag agaaagacat cttctaaata acaaataagga ggagttacag tacctgactt 120
37 ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180
38 gcggagaagg attccgaaga cgaagaaaat atccttagag atccaagcta agtgtagtgc 240
39 agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagttagga 300
40 gtctctctga gggtctggctt tgtgagccac agtgatttgt aacttaatgc gaactaattt 360
41 gctgttagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412
42 Met Met Ser Cys Trp Phe Ser
43 1 5
45 tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460
46 Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
47 10 15 20
49 cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508
50 Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
51 25 30 35
53 atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556
54 Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
55 40 45 50 55
57 aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604
58 Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
59 60 65 70
61 aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652
62 Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Thr Ser Asp Thr Ala
63 75 80 85
65 gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt 700
66 Gly Arg Asn Ala Leu His Leu Ala Ala Lys Tyr Gly His Ala Leu Cys

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67	90	95	100	
69	cta	caa	aaa	ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748
70	Leu	Gln	Lys	Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu
71	105	110	115	
73	cag	gga	aga	act gca ctt cat gat gca gct atg gca gac tgt cct tct 796
74	Gln	Gly	Arg	Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser
75	120	125	130	135
77	agc	ata	cag	ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844
78	Ser	Ile	Gln	Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp
79	140	145	150	
81	gta	gat	ggg	cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca 892
82	Val	Asp	Gly	Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro
83	155	160	165	
85	aca	ata	tgt	caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga 940
86	Thr	Ile	Cys	Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg
87	170	175	180	
89	gac	aaa	caa	aac agg act gct ctc atg cta gga tgc gag tat ggt tgc 988
90	Asp	Lys	Gln	Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys
91	185	190	195	
93	aaa	gat	gca	gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg 1036
94	Lys	Asp	Ala	Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu
95	200	205	210	215
97	ctg	gac	gcc	ctt ggc cat gac agt tct tac tat gca aga att ggt gac 1084
98	Leu	Asp	Ala	Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp
99	220	225	230	
101	aat	ctg	gac	att cta acc tta ctg aag act gca tca gaa aat tcc aac 1132
102	Asn	Leu	Asp	Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn
103	235	240	245	
105	aaa	ggg	aga	gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat 1180
106	Lys	Gly	Arg	Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn
107	250	255	260	
109	ttg	tct	cag	atg cta gat gaa gta aat acg aag tca aat cag agg gag 1228
110	Leu	Ser	Gln	Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu
111	265	270	275	
113	cat	caa	aac	att cag gat ctg gag att gaa aat gaa gat ctg aaa gag 1276
114	His	Gln	Asn	Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu
115	280	285	290	295
117	aga	ttg	aga	aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc 1324
118	Arg	Leu	Arg	Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val
119	300	305	310	
121	aat	ggt	tta	cag cta cag ctg aat gag gaa gta atg gtg gct gat gat 1372
122	Asn	Gly	Leu	Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp
123	315	320	325	
125	ctg	gaa	agt	gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa 1420
126	Leu	Glu	Ser	Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu
127	330	335	340	
129	aag	cag	cat	gaa gaa agc cta aga act att gag gct ctg aaa agt aga 1468
130	Lys	Gln	His	Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg
131	345	350	355	

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133 ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg 1516
134 Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg
135 360 365 370 375
137 aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca 1564
138 Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser
139 380 385 390
141 cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg 1612
142 Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met
143 395 400 405
145 tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa 1660
146 Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu
147 410 415 420
149 aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat 1708
150 Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp
151 425 430 435
153 tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag 1756
154 Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys
155 440 445 450 455
157 gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag 1804
158 Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu
159 460 465 470
161 gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg 1852
162 Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val
163 475 480 485
165 cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca 1900
166 Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr
167 490 495 500
169 cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg 1948
170 His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly
171 505 510 515
173 aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa 1996
174 Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys
175 520 525 530 535
177 gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa 2044
178 Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln
179 540 545 550
181 atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc 2092
182 Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly
183 555 560 565
185 aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt 2140
186 Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys
187 570 575 580
189 gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc 2188
190 Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly
191 585 590 595
193 cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag 2236
194 Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu
195 600 605 610 615
197 aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag 2284

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198 Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys
199                               620                               625                               630
201 gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat 2332
202 Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn
203                               635                               640                               645
205 gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg 2380
206 Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu
207                               650                               655                               660
209 gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta 2428
210 Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu
211                               665                               670                               675
213 gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg 2476
214 Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser
215 680                               685                               690                               695
217 aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat 2524
218 Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn
219                               700                               705                               710
221 aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat 2572
222 Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn
223                               715                               720                               725
225 gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat gta att 2620
226 Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp Val Ile
227                               730                               735                               740
229 gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa tat aca 2668
230 Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys Tyr Thr
231                               745                               750                               755
233 gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc agt tta 2716
234 Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala Ser Leu
235 760                               765                               770                               775
237 agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc gag aga 2764
238 Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro Glu Arg
239                               780                               785                               790
241 cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa ctt aag 2812
242 His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu Leu Lys
243                               795                               800                               805
245 aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa gag aaa 2860
246 Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln Glu Lys
247                               810                               815                               820
249 ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc atg agt 2908
250 Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr Met Ser
251                               825                               830                               835
253 cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act gcc ttg 2956
254 His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr Ala Leu
255 840                               845                               850                               855
257 agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg aag aag 3004
258 Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val Lys Lys
259                               860                               865                               870
261 aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat gag aac 3052
262 Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp Glu Asn

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263	875	880	885	
265 gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta aaa gct				3100
266 Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val Lys Ala				
267	890	895	900	
269 gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc cta agg				3148
270 Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly Leu Arg				
271	905	910	915	
273 aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg gct aag				3196
274 Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu Ala Lys				
275 920	925	930	935	
277 tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag att gca				3244
278 Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu Ile Ala				
279	940	945	950	
281 gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag cta aaa				3292
282 Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys Leu Lys				
283	955	960	965	
285 tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt aaa gcc				3340
286 Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe Lys Ala				
287	970	975	980	
289 act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag aag tat				3388
290 Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln Lys Tyr				
291	985	990	995	
293 aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat gac aag				3436
294 Asn Thr Ser Glu Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn Asp Lys				
295 1000	1005	1010	1015	
297 tta aag aag gag atc ctc act ctt cag aag gat cta aag gat aag aat				3484
298 Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp Lys Asn				
299	1020	1025	1030	
301 gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc aga aaa				3532
302 Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser Arg Lys				
303	1035	1040	1045	
305 aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa tac aca				3580
306 Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys Tyr Thr				
307	1050	1055	1060	
309 gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc aag cag				3628
310 Glu Ala Lys Lys Glu Lys Glu Lys Leu Val Glu Glu Asn Ala Lys Gln				
311	1065	1070	1075	
313 act tct gag atc ctt gca gca caa act ctt ttg cag aag cag cat gtt				3676
314 Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln His Val				
315 1080	1085	1090	1095	
317 ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt aca atc				3724
318 Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly Thr Ile				
319	1100	1105	1110	
321 gag aca ctc aag gaa gaa ctg aaa act aag cag aga tgt tat gag aaa				3772
322 Glu Thr Leu Lys Glu Glu Leu Lys Thr Lys Gln Arg Cys Tyr Glu Lys				
323	1115	1120	1125	
325 gag cag cag aca gtg acc caa ctg cgg cag atg ctg gag aat cag aag				3820
326 Glu Gln Gln Thr Val Thr Gln Leu Arg Gln Met Leu Glu Asn Gln Lys				
327	1130	1135	1140	

VERIFICATION SUMMARY

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